

## SEQUENCE LISTING

<110> Kindsvogel, Wayne R.  
Topouzis, Stavros

<120> SOLUBLE ZCYTOR11 CYTOKINE RECEPTORS

<130> 00-56

<150> US 60/223,827

<151> 2000-08-08

<150> US 60/250,876

<151> 2000-12-01

<160> 35

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 2831

<212> DNA

<213> Homo sapien

<220>

<221> CDS

<222> (34)...(1755)

<400> 1

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Met Arg Thr Leu Leu Thr Ile

1

5

ttg act atg gga tcc ctg gct gct cac gcc cct gag gac ccc tcg gat 102

Leu Thr Val Gly Ser Leu Ala Ala His Ala Pro Glu Asp Pro Ser Asp

10

15

20

ctg ctc cag cac gtg aaa ttc cag tcc agc aac ttt gaa aac atc ctg 150

Leu Leu Gln His Val Lys Phe Gln Ser Ser Asn Phe Glu Asn Ile Leu

25

30

35

acg tgg gac agc ggg cca gag ggc acc cca gac acg gtc tac agc atc 198



atg tgc cga gtg aag aca ctg cca gac cgg aca tgg acc tac tcc ttc	726
Met Cys Arg Val Lys Thr Leu Pro Asp Arg Thr Trp Thr Tyr Ser Phe	
220 225 230	
ccc gga gcc ttc ctg ttc tcc atg ggc ttc ctc gtc gca gta ctc tgc	774
Ser Gly Ala Phe Leu Phe Ser Met Gly Phe Leu Val Ala Val Leu Cys	
235 240 245	
tac ctg agc tac aga tat gtc acc aag ccg cct gca cct ccc aac tcc	822
Tyr Leu Ser Tyr Arg Tyr Val Thr Lys Pro Pro Ala Pro Pro Asn Ser	
250 255 260	
ctg aac gtc cag cga gtc ctg act ttc cag ccg ctg cgc ttc atc cag	870
Leu Asn Val Gln Arg Val Leu Thr Phe Gln Pro Leu Arg Phe Ile Gln	
265 270 275	
gag cac gtc ctg atc cct gtc ttt gac ctc agc ggc ccc agc agt ctg	918
Glu His Val Leu Ile Pro Val Phe Asp Leu Ser Gly Pro Ser Ser Leu	
280 285 290 295	
gcc cag cct gtc cag tac tcc cag atc agg gtg tct gga ccc agg gag	966
Ala Gln Pro Val Gln Tyr Ser Gln Ile Arg Val Ser Gly Pro Arg Glu	
300 305 310	
ccc gca gga gct cca cag cgg cat agc ctg tcc gag atc acc tac tta	1014
Pro Ala Gly Ala Pro Gln Arg His Ser Leu Ser Glu Ile Thr Tyr Leu	
315 320 325	
ggg cag cca gac atc tcc atc ctc cag ccc tcc aac gtg cca cct ccc	1062
Gly Gln Pro Asp Ile Ser Ile Leu Gln Pro Ser Asn Val Pro Pro Pro	
330 335 340	
cag atc ctc tcc cca ctg tcc tat gcc cca aac gct gcc cct gag gtc	1110
Gln Ile Leu Ser Pro Leu Ser Tyr Ala Pro Asn Ala Ala Pro Glu Val	
345 350 355	
ggg ccc cca tcc tat gca cct cag gtg acc ccc gaa gct caa ttc cca	1158
Gly Pro Pro Ser Tyr Ala Pro Gln Val Thr Pro Glu Ala Gln Phe Pro	
360 365 370 375	
ttc tac gcc cca cag gcc atc tct aag gtc cag cct tcc tcc tat gcc	1206
Phe Tyr Ala Pro Gln Ala Ile Ser Lys Val Gln Pro Ser Ser Tyr Ala	
380 385 390	

cct caa gcc act ccg gac agc tgg cct ccc tcc tat ggg gta tgc atg Pro Gln Ala Thr Pro Asp Ser Trp Pro Pro Ser Tyr Gly Val Cys Met 395 400 405	1254
gaa ggt tct ggc aaa gac tcc ccc act ggg aca ctt tct agt cct aaa Glu Gly Ser Gly Lys Asp Ser Pro Thr Gly Thr Leu Ser Ser Pro Lys 410 415 420	1302
cac ctt agg cct aaa ggt cag ctt cag aaa gag cca cca gct gga agc His Leu Arg Pro Lys Gly Gln Leu Gln Lys Glu Pro Pro Ala Gly Ser 425 430 435	1350
tgc atg tta ggt ggc ctt tct ctg cag gag gtg acc tcc ttg gct atg Cys Met Leu Gly Gly Leu Ser Leu Gln Glu Val Thr Ser Leu Ala Met 440 445 450 455	1398
gag gaa tcc caa gaa gca aaa tca ttg cac cag ccc ctg ggg att tgc Glu Glu Ser Gln Glu Ala Lys Ser Leu His Gln Pro Leu Gly Ile Cys 460 465 470	1446
aca gac aga aca tct gac cca aat gtg cta cac agt ggg gag gaa ggg Thr Asp Arg Thr Ser Asp Pro Asn Val Leu His Ser Gly Glu Glu Gly 475 480 485	1494
aca cca cag tac cta aag ggc cag ctc ccc ctc ctc tcc tca gtc cag Thr Pro Gln Tyr Leu Lys Gly Gln Leu Pro Leu Leu Ser Ser Val Gln 490 495 500	1542
atc gag ggc cac ccc atg tcc ctc cct ctg caa cct cct tcc ggt cca Ile Glu Gly His Pro Met Ser Leu Pro Leu Gln Pro Pro Ser Gly Pro 505 510 515	1590
tgt tcc ccc tcc gac caa ggt cca agt ccc tgg ggc ctg ctg gag tcc Cys Ser Pro Ser Asp Gln Gly Pro Ser Pro Trp Gly Leu Leu Glu Ser 520 525 530 535	1638
ctt gtg tgt ccc aag gat gaa gcc aag agc cca gcc cct gag acc tca Leu Val Cys Pro Lys Asp Glu Ala Lys Ser Pro Ala Pro Glu Thr Ser 540 545 550	1686
gac ctg gag cag ccc aca gaa ctg gat tct ctt ttc aga ggc ctg gcc	1734

Asp Leu Glu Gln Pro Thr Glu Leu Asp Ser Leu Phe Arg Gly Leu Ala  
 555 560 565

ctg act gtg cag tgg gag tcc tgaggggaat gggaaaggct tgggtgcttcc 1785  
 Leu Thr Val Gln Trp Glu Ser  
 570

tcctgtgcc taccagtggt cacatccttg gctgtcaatc ccatgectgc ccatgccaca 1845  
 cactctgga tctggcctca gacgggtgcc cttgagagaa gcagagggag tggcatgcag 1905  
 ggcccttgc atgggtgggc tcttcaccgg aacaaagcag catgataagg actgcagcgg 1965  
 gggagctctg gggagcagct tgtgtagaca agcgcgtgct cgtgagccc tgcaaggcag 2025  
 aatgacagt gcaaggagga aatgcaggga aactcccgag gtccagagcc ccacctccta 2085  
 acaccatgga ttcaaagtgc tcagggaatt tgcctcctc tgcctcctc ctggccagtt 2145  
 tcacaatcta gctcgacaga gcctgaggcc cctgcctctt ctgtcattgt tcaaaggtgg 2205  
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 gtgtggcctg cagctcattc ccagccaggg caactgcctg acgttgcacg atttcagctt 2385  
 cattcctctg atagaacaaa gcgaaatgca ggctccaccg ggagggagac acacaagcct 2445  
 tttctgcagg caggagtttc agacctatc ctgagaatgg ggtttgaaag gaaggtgagg 2505  
 gctgtggccc ctggacgggt acaataaac acgtgtactga tgtcacaact ttgcaagctc 2565  
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 cttcaaacaa atgaaatcag tgcccagaac ctcggtttcc tcactctgtaa tgtggggatc 2685  
 ataacacctt cctcatggag ttgtgggtgaa gatgaaatga agtcatgtct ttaaagtgtc 2745  
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 aaaaaaaaaa atagcgggcg cctcga 2831

<210> 2

<211> 574

<212> PRT

<213> Homo sapien

<400> 1

Met Arg Thr Leu Leu Thr Ile Leu Thr Val Gly Ser Leu Ala Ala His  
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 Ala Pro Glu Asp Pro Ser Asp Leu Leu Gln His Val Lys Phe Gln Ser  
 20 25 30  
 Ser Asn Phe Glu Asn Ile Leu Thr Trp Asp Ser Gly Pro Glu Gly Thr  
 35 40 45  
 Pro Asp Thr Val Tyr Ser Ile Glu Tyr Lys Thr Tyr Gly Glu Arg Asp  
 50 55 60  
 Trp Val Ala Lys Lys Gly Cys Gln Arg Ile Thr Arg Lys Ser Cys Asn  
 65 70 75 80

Leu Thr Val Glu Thr Gly Asn Leu Thr Glu Leu Tyr Tyr Ala Arg Val  
                     85                    90                    95  
 Thr Ala Val Ser Ala Gly Gly Arg Ser Ala Thr Lys Met Thr Asp Arg  
                     100                    105                    110  
 Phe Ser Ser Leu Gln His Thr Thr Leu Lys Pro Pro Asp Val Thr Cys  
                     115                    120                    125  
 Ile Ser Lys Val Arg Ser Ile Gln Met Ile Val His Pro Thr Pro Thr  
                     130                    135                    140  
 Pro Ile Arg Ala Gly Asp Gly His Arg Leu Thr Leu Glu Asp Ile Phe  
 145                    150                    155                    160  
 His Asp Leu Phe Tyr His Leu Glu Leu Gln Val Asn Arg Thr Tyr Gln  
                     165                    170                    175  
 Met His Leu Gly Gly Lys Gln Arg Glu Tyr Glu Phe Phe Gly Leu Thr  
                     180                    185                    190  
 Pro Asp Thr Glu Phe Leu Gly Thr Ile Met Ile Cys Val Pro Thr Trp  
                     195                    200                    205  
 Ala Lys Glu Ser Ala Pro Tyr Met Cys Arg Val Lys Thr Leu Pro Asp  
                     210                    215                    220  
 Arg Thr Trp Thr Tyr Ser Phe Ser Gly Ala Phe Leu Phe Ser Met Gly  
 225                    230                    235                    240  
 Phe Leu Val Ala Val Leu Cys Tyr Leu Ser Tyr Arg Tyr Val Thr Lys  
                     245                    250                    255  
 Pro Pro Ala Pro Pro Asn Ser Leu Asn Val Gln Arg Val Leu Thr Phe  
                     260                    265                    270  
 Gln Pro Leu Arg Phe Ile Gln Glu His Val Leu Ile Pro Val Phe Asp  
                     275                    280                    285  
 Leu Ser Gly Pro Ser Ser Leu Ala Gln Pro Val Gln Tyr Ser Gln Ile  
                     290                    295                    300  
 Arg Val Ser Gly Pro Arg Glu Pro Ala Gly Ala Pro Gln Arg His Ser  
 305                    310                    315                    320  
 Leu Ser Glu Ile Thr Tyr Leu Gly Gln Pro Asp Ile Ser Ile Leu Gln  
                     325                    330                    335  
 Pro Ser Asn Val Pro Pro Pro Gln Ile Leu Ser Pro Leu Ser Tyr Ala  
                     340                    345                    350  
 Pro Asn Ala Ala Pro Glu Val Gly Pro Pro Ser Tyr Ala Pro Gln Val  
                     355                    360                    365  
 Thr Pro Glu Ala Gln Phe Pro Phe Tyr Ala Pro Gln Ala Ile Ser Lys  
                     370                    375                    380  
 Val Gln Pro Ser Ser Tyr Ala Pro Gln Ala Thr Pro Asp Ser Trp Pro  
 385                    390                    395                    400  
 Pro Ser Tyr Gly Val Cys Met Glu Gly Ser Gly Lys Asp Ser Pro Thr  
                     405                    410                    415

Gly Thr Leu Ser Ser Pro Lys His Leu Arg Pro Lys Gly Gln Leu Gln  
                   420                  425                  430  
 Lys Glu Pro Pro Ala Gly Ser Cys Met Leu Gly Gly Leu Ser Leu Gln  
                   435                  440                  445  
 Glu Val Thr Ser Leu Ala Met Glu Glu Ser Gln Glu Ala Lys Ser Leu  
                   450                  455                  460  
 His Gln Pro Leu Gly Ile Cys Thr Asp Arg Thr Ser Asp Pro Asn Val  
 465                  470                  475                  480  
 Leu His Ser Gly Glu Glu Gly Thr Pro Gln Tyr Leu Lys Gly Gln Leu  
                   485                  490                  495  
 Pro Leu Leu Ser Ser Val Gln Ile Glu Gly His Pro Met Ser Leu Pro  
                   500                  505                  510  
 Leu Gln Pro Pro Ser Gly Pro Cys Ser Pro Ser Asp Gln Gly Pro Ser  
                   515                  520                  525  
 Pro Trp Gly Leu Leu Glu Ser Leu Val Cys Pro Lys Asp Glu Ala Lys  
                   530                  535                  540  
 Ser Pro Ala Pro Glu Thr Ser Asp Leu Glu Gln Pro Thr Glu Leu Asp  
 545                  550                  555                  560  
 Ser Leu Phe Arg Gly Leu Ala Leu Thr Val Gln Trp Glu Ser  
                   565                  570

&lt;210&gt; 3

&lt;211&gt; 211

&lt;212&gt; FRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3

Pro Glu Asp Pro Ser Asp Leu Leu Gln His Val Lys Phe Gln Ser Ser  
 1                  5                  10                  15  
 Asn Phe Glu Asn Ile Leu Thr Trp Asp Ser Gly Pro Glu Gly Thr Pro  
                   20                  25                  30  
 Asp Thr Val Tyr Ser Ile Glu Tyr Lys Thr Tyr Gly Glu Arg Asp Trp  
                   35                  40                  45  
 Val Ala Lys Lys Gly Cys Gln Arg Ile Thr Arg Lys Ser Cys Asn Leu  
                   50                  55                  60  
 Thr Val Glu Thr Gly Asn Leu Thr Glu Leu Tyr Tyr Ala Arg Val Thr  
 65                  70                  75                  80  
 Ala Val Ser Ala Gly Gly Arg Ser Ala Thr Lys Met Thr Asp Arg Phe  
                   85                  90                  95  
 Ser Ser Leu Gln His Thr Thr Leu Lys Pro Pro Asp Val Thr Cys Ile  
                   100                  105                  110

Ser Lys Val Arg Ser Ile Gln Met Ile Val His Pro Thr Pro Thr Pro  
 115 120 125  
 Ile Arg Ala Gly Asp Gly His Arg Leu Thr Leu Glu Asp Ile Phe His  
 130 135 140  
 Asp Leu Phe Tyr His Leu Glu Leu Gln Val Asn Arg Thr Tyr Gln Met  
 145 150 155 160  
 His Leu Gly Gly Lys Gln Arg Glu Tyr Glu Phe Phe Gly Leu Thr Pro  
 165 170 175  
 Asp Thr Glu Phe Leu Gly Thr Ile Met Ile Cys Val Pro Thr Trp Ala  
 180 185 190  
 Lys Glu Ser Ala Pro Tyr Met Cys Arg Val Lys Thr Leu Pro Asp Arg  
 195 200 205  
 Thr Trp Thr  
 210

<210> 4  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Glu-Glu peptide tag

<400> 4  
 Glu Tyr Met Pro Met Glu  
 1 5

<210> 5  
 <211> 8  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Flag-tag peptide

<400> 5  
 Asp Tyr Lys Asp Asp Asp Asp Lys  
 1 5

<210> 6  
 <211> 699  
 <212> DNA



&lt;213&gt; Homo sapiens

&lt;400&gt; 6

gagcccaqat cttcagacaa aactcacaca tgcccaccgt gccccagcacc tgaagccgag	60
ggggcaccgt cagtcttctt cttcccccca aaacccaagg acacctctat gatctcccgg	120
acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagacctga ggtcaagttc	180
aactggtaag tggacggcgt ggaggtgcat aatgccaaaga caaagccgcg ggaggagcag	240
tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat	300
ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc catctccat cgagaaaacc	360
atctccaaag ccaaagggca gccccgagaa ccacaggtgt acacctgcc cccatcccgg	420
gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc	480
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct	540
cccgtgctgg actccgacgg ctctttcttc ctctacagca agctcaccgt ggacaagagc	600
aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac	660
tacacgcaga agagcctctc cctgtctccg ggtaaataa	699

&lt;210&gt; 7

&lt;211&gt; 1116

&lt;212&gt; DNA

&lt;213&gt; homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (21)...(557)

&lt;400&gt; 7

tcgagttaga attgtctgca atg gcc gcc ctg cag aaa tct gtg agc tct ttc	53
Met Ala Ala Leu Gln Lys Ser Val Ser Ser Phe	
1 5 10	
ctt atg ggg acc ctg gcc acc agc tgc ctc ctt ctc ttg gcc ctc ttg	101
Leu Met Gly Thr Leu Ala Thr Ser Cys Leu Leu Leu Ala Leu Leu	
15 20 25	
gta cag gga gga gca gct ggg ccc atc agc tcc cac tgc agg ctt gac	149
Val Gln Gly Gly Ala Ala Ala Pro Ile Ser Ser His Cys Arg Leu Asp	
30 35 40	
aag tcc aac ttc cag cag ccc tat atc acc aac cgc acc ttc atg ctg	197
Lys Ser Asn Phe Gln Gln Pro Tyr Ile Thr Asn Arg Thr Phe Met Leu	
45 50 55	
gct aag gag gct agc ttg gct gat aac aac aca gac gtt cgt ctc att	245



&lt;212&gt; PRT

&lt;213&gt; homo sapiens

&lt;400&gt; 8

Met Ala A'a Leu Gln Lys Ser Val Ser Ser Phe Leu Met Gly Thr Leu  
 1 5 10 15  
 Ala Thr Ser Cys Leu Leu Leu Leu Ala Leu Leu Val Gln Gly Gly Ala  
 20 25 30  
 Ala Ala Pro Ile Ser Ser His Cys Arg Leu Asp Lys Ser Asn Phe Gln  
 35 40 45  
 Gln Pro Tyr Ile Thr Asn Arg Thr Phe Met Leu Ala Lys Glu Ala Ser  
 50 55 60  
 Leu Ala Asp Asn Asn Thr Asp Val Arg Leu Ile Gly Glu Lys Leu Phe  
 65 70 75 80  
 His Gly Val Ser Met Ser Glu Arg Cys Tyr Leu Met Lys Gln Val Leu  
 85 90 95  
 Asn Phe Thr Leu Glu Glu Val Leu Phe Pro Gln Ser Asp Arg Phe Gln  
 100 105 110  
 Pro Tyr Met Gln Glu Val Val Pro Phe Leu Ala Arg Leu Ser Asn Arg  
 115 120 125  
 Leu Ser Thr Cys His Ile Glu Gly Asp Asp Leu His Ile Gln Arg Asn  
 130 135 140  
 Val Gln Lys Leu Lys Asp Thr Val Lys Lys Leu Gly Glu Ser Gly Glu  
 145 150 155 160  
 Ile Lys Ala Ile Gly Glu Leu Asp Leu Leu Phe Met Ser Leu Arg Asn  
 165 170 175  
 Ala Cys Ile

&lt;210&gt; 9

&lt;211&gt; 36

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Oligonucleotide prime ZC28590

&lt;400&gt; 9

ttgggtacct ctgcaatggc cgcctgtcag aaatct

36

&lt;210&gt; 10

&lt;211&gt; 33

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Oligonucleotide prime ZC28580

&lt;400&gt; 10

ttgggatcca atgcaggcat ttctcagaga cat

33

&lt;210&gt; 11

&lt;211&gt; 18

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Oligonucleotide prime ZC14666

&lt;400&gt; 11

agccaccaag atgactga

18

&lt;210&gt; 12

&lt;211&gt; 22

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Oligonucleotide prime ZC14742

&lt;400&gt; 12

tgcatttggt aggtgcggtt ga

22

&lt;210&gt; 13

&lt;211&gt; 6

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; His tag

&lt;400&gt; 13

His His His His His His

1

5

&lt;210&gt; 14

&lt;211&gt; 63

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC29239

<400> 14

gaggccagat ccggttcggg ttgggttcg gagccagat catcagacaa aactcacaca 60  
tgc 63

<210> 15

<211> 65

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC29232

<400> 15

cgactgactc gagtcagtga tggatgatgg gatggccacc tgatccttta cccggagaca 60  
gggag 65

<210> 16

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC39319

<400> 16

atcggaattc gcagaagcca tggcgtggag ccttggg 37

<210> 17

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC39325

<400> 17

cagtggatnc ggaggggacc gtttcgtc 28

<210> 18  
 <211> 660  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(660)

<400> 18

atg gcg tgg agt ctt ggg agc tgg ctg ggt ggc tgc ctg ctg gtg tca	48
Met Ala Trp Ser Leu Gly Ser Trp Leu Gly Gly Cys Leu Leu Val Ser	
1 5 10 15	

gca ttg gga atg gta cca cct ccc gaa aat gtc aga atg aat tct gtt	96
Ala Leu Gly Met Val Pro Pro Pro Glu Asn Val Arg Met Asn Ser Val	
20 25 30	

aat ttc aag aac att cta cag tgg gag tca cct gct ttt gcc aaa ggg	144
Asn Phe Lys Asn Ile Leu Gln Trp Glu Ser Pro Ala Phe Ala Lys Gly	
35 40 45	

aac ctg act ttc aca gct cag tac cta agt tat agg ata ttc caa gat	192
Asn Leu Thr Phe Thr Ala Gln Tyr Leu Ser Tyr Arg Ile Phe Gln Asp	
50 55 60	

aaa tgc atg aat act acc ttg acg gaa tgt gat ttc tca agt ctt tcc	240
Lys Cys Met Asn Thr Thr Leu Thr Glu Cys Asp Phe Ser Ser Leu Ser	
65 70 75 80	

aag tat ggt gac cac acc ttg aga gtc agg gct gaa ttt gca gat gag	288
Lys Tyr Gly Asp His Thr Leu Arg Val Arg Ala Glu Phe Ala Asp Glu	
85 90 95	

cat tca gac tgg gta aac atc acc ttc tgt cct gtg gat gac acc att	336
His Ser Asp Trp Val Asn Ile Thr Phe Cys Pro Val Asp Asp Thr Ile	
100 105 110	

att gga ccc cct gga atg caa gta gaa gta ctt gat gat tct tta cat	384
Ile Gly Pro Pro Gly Met Gln Val Glu Val Leu Asp Asp Ser Leu His	
115 120 125	

atg cgt ttc tta gcc cct aaa att gag aat gaa tac gaa act tgg act 432  
 Met Arg Phe Leu Ala Pro Lys Ile Glu Asn Glu Tyr Glu Thr Trp Thr  
 130 135 140

atg aag aat gtg tat aac tca tgg act tat aat gtg caa tac tgg aaa 480  
 Met Lys Asn Val Tyr Asn Ser Trp Thr Tyr Asn Val Gln Tyr Trp Lys  
 145 150 155 160

aac ggt act gat gaa aag ttt caa att act ccc cag tat gac ttt gag 528  
 Asn Gly Thr Asp Glu Lys Phe Gln Ile Thr Pro Gln Tyr Asp Phe Glu  
 165 170 175

gtc ctc aga aac ctg gag cca tgg aca act tat tgt gtt caa gtt cga 576  
 Val Leu Arg Asn Leu Glu Pro Trp Thr Thr Tyr Cys Val Gln Val Arg  
 180 185 190

ggg ttt ctt cct gat cgg aac aaa gct ggg gaa tgg agt gag cct gtc 624  
 Gly Phe Leu Pro Asp Arg Asn Lys Ala Gly Glu Trp Ser Glu Pro Val  
 195 200 205

tgt gag caa aca acc cat gac gaa acg gtc ccc tcc 660  
 Cys Glu Gln Thr Thr His Asp Glu Thr Val Pro Ser  
 210 215 220

<210> 19

<211> 220

<212> PRT

<213> Homo sapiens

<400> 19

Met Ala Trp Ser Leu Gly Ser Trp Leu Gly Gly Cys Leu Leu Val Ser  
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 Ala Leu Gly Met Val Pro Pro Pro Glu Asn Val Arg Met Asn Ser Val  
 20 25 30  
 Asn Phe Lys Asn Ile Leu Gln Trp Glu Ser Pro Ala Phe Ala Lys Gly  
 35 40 45  
 Asn Leu Thr Phe Thr Ala Gln Tyr Leu Ser Tyr Arg Ile Phe Gln Asp  
 50 55 60  
 Lys Cys Met Asn Thr Thr Leu Thr Glu Cys Asp Phe Ser Ser Leu Ser  
 65 70 75 80  
 Lys Tyr Gly Asp His Thr Leu Arg Val Arg Ala Glu Phe Ala Asp Glu  
 85 90 95

His Ser Asp Trp Val Asn Ile Thr Phe Cys Pro Val Asp Asp Thr Ile  
           100                          105                          110  
 Ile Gly Pro Pro Gly Met Gln Val Glu Val Leu Asp Asp Ser Leu His  
           115                          120                          125  
 Met Arg Phe Leu Ala Pro Lys Ile Glu Asn Glu Tyr Glu Thr Trp Thr  
           130                          135                          140  
 Met Lys Asn Val Tyr Asn Ser Trp Thr Tyr Asn Val Gln Tyr Trp Lys  
           145                          150                          155                          160  
 Asn Gly Thr Asp Glu Lys Phe Gln Ile Thr Pro Gln Tyr Asp Phe Glu  
                           165                          170                          175  
 Val Leu Arg Asn Leu Glu Pro Trp Thr Thr Tyr Cys Val Gln Val Arg  
                           180                          185                          190  
 Gly Phe Leu Pro Asp Arg Asn Lys Ala Gly Glu Trp Ser Glu Pro Val  
           195                          200                          205  
 Cys Glu Gln Thr Thr His Asp Glu Thr Val Pro Ser  
           210                          215                          220

&lt;210&gt; 20

&lt;211&gt; 18

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Oligonucleotide primer ZC38931

&lt;400&gt; 20

acaaagccgc gggaggag

18

&lt;210&gt; 21

&lt;211&gt; 82

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Oligonucleotide primer ZC39042

&lt;400&gt; 21

ctgactcag ttagtgatgg tgatggtgat ggccacctga tccggaacca cgcggaacca  
 gtttacccg agacaggag ag

60

82

&lt;210&gt; 22

&lt;211&gt; 1428



&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(1428)

<223> CRF2-4 extracellular cytokine binding domain fused  
to IgGg1 with a 6-HIS tag

&lt;400&gt; 22

atg gcg tgg agt ctt ggg agc tgg ctg ggt ggc tgc ctg ctg gtg tca	48
Met Ala Trp Ser Leu Gly Ser Trp Leu Gly Gly Cys Leu Leu Val Ser	
1 5 10 15	
gca ttg gga atg gta cca cct ccc gaa aat gtc aga atg aat tct gtt	96
Ala Leu Gly Met Val Pro Pro Pro Glu Asn Val Arg Met Asn Ser Val	
20 25 30	
aat ttc aag aac att cta cag tgg gag tca cct gct ttt gcc aaa ggg	144
Asn Phe Lys Asn Ile Leu Gln Trp Glu Ser Pro Ala Phe Ala Lys Gly	
35 40 45	
aac ctg act ttc aca gct cag tac cta agt tat agg ata ttc caa gat	192
Asn Leu Thr Phe Thr Ala Gln Tyr Leu Ser Tyr Arg Ile Phe Gln Asp	
50 55 60	
aaa tgc atg aat act acc ttg acg gaa tgt gat ttc tca agt ctt tcc	240
Lys Cys Met Asn Thr Thr Leu Thr Glu Cys Asp Phe Ser Ser Leu Ser	
65 70 75 80	
aag tat ggt gac cac acc ttg aga gtc agg gct gaa ttt gca gat gag	288
Lys Tyr Gly Asp His Thr Leu Arg Val Arg Ala Glu Phe Ala Asp Glu	
85 90 95	
cat tca gac tgg gta aac atc acc ttc tgt cct gtg gat gac acc att	336
His Ser Asp Trp Val Asn Ile Thr Phe Cys Pro Val Asp Asp Thr Ile	
100 105 110	
att gga ccc cct gga atg caa gta gaa gta ctt gat gat tct tta cat	384
Ile Gly Pro Pro Gly Met Gln Val Glu Val Leu Asp Asp Ser Leu His	
115 120 125	

atg cgt ttc tta gcc cct aaa att gag aat gaa tac gaa act tgg act	432
Met Arg Phe Leu Ala Pro Lys Ile Glu Asn Glu Tyr Glu Thr Trp Thr	
130 135 140	
atg aag aat gtg tat aac tca tgg act tat aat gtg caa tac tgg aaa	480
Met Lys Asn Val Tyr Asn Ser Trp Thr Tyr Asn Val Gln Tyr Trp Lys	
145 150 155 160	
aac ggt act gat gaa aag ttt caa att act ccc cag tat gac ttt gag	528
Asn Gly Thr Asp Glu Lys Phe Gln Ile Thr Pro Gln Tyr Asp Phe Glu	
165 170 175	
gtc ctc aga aac ctg gag cca tgg aca act tat tgt gtt caa gtt cga	576
Val Leu Arg Asn Leu Glu Pro Trp Thr Thr Tyr Cys Val Gln Val Arg	
180 185 190	
ggg ttt ctt cct gat cgg aac aaa gct ggg gaa tgg agt gag cct gtc	624
Gly Phe Leu Pro Asp Arg Asn Lys Ala Gly Glu Trp Ser Glu Pro Val	
195 200 205	
tgt gag caa aca acc cat gac gaa acg gtc ccc tcc gga tcc ggt tgg	672
Cys Glu Gln Thr Thr His Asp Glu Thr Val Pro Ser Gly Ser Gly Ser	
210 215 220	
ggt tgg ggt tgg gag ccc aga tca tca gac aaa act cac aca tgc cca	720
Gly Ser Gly Ser Glu Pro Arg Ser Ser Asp Lys Thr His Thr Cys Pro	
225 230 235 240	
cgg tgc cca gca cct gaa gcc gag ggg gca cgg tca gtc ttc ctc ttc	768
Pro Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe	
245 250 255	
ccc cca aaa ccc aag gac acc ctc atg atc tcc cgg acc cct gag gtc	816
Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val	
260 265 270	
aaa tgc gtg gtg gtg gac gtg agc cac gaa gac cct gag gtc aag ttc	864
Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe	
275 280 285	
aac tgg tac gtg gac ggc gtg gag gtg cat aat gcc aag aca aag cgg	912
Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro	
290 295 300	

egg gag gag cag tac aac agc acg tac cgt gtg gtc agc gtc ctc acc	960
Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr	
305 310 315 320	
gtc ctg cac cag gac tgg ctg aat ggc aag gag tac aag tgc aag gtc	1008
Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val	
325 330 335	
tcc aac aaa gcc ctc cca tcc tcc atc gag aaa acc atc tcc aaa gcc	1056
Ser Asn Lys Ala Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala	
340 345 350	
aaa ggg cag ccc cga gaa cca cag gtg tac acc ctg ccc cca tcc cgg	1104
Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg	
355 360 365	
gat gag ctg acc aag aac cag gtc agc ctg acc tgc ctg gtc aaa ggc	1152
Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly	
370 375 380	
ttc tat ccc agc gac atc gcc gtg gag tgg gag agc aat ggg cag ccg	1200
Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro	
385 390 395 400	
gag aac aac tac aag acc acg cct ccc gtg ctg gac tcc gac ggc tcc	1248
Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser	
405 410 415	
ttc ttc ctc tac agc aag ctc acc gtg gac aag agc agg tgg cag cag	1296
Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln	
420 425 430	
ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct ctg cac aac cac	1344
Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His	
435 440 445	
tac acg cag aag agc ctc tcc ctg tct ccg ggt aaa ctg gtt ccg cgt	1392
Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Leu Val Pro Arg	
450 455 460	
ggt tcc gga tca ggt ggc cat cac cat cac cat cac	1428

Gly Ser Gly Ser Gly Gly His His His His His His  
 465 470 475

<210> 23  
 <211> 476  
 <212> PRT  
 <213> Homo sapiens

<400> 23

Met	Ala	Trp	Ser	Leu	Gly	Ser	Trp	Leu	Gly	Gly	Cys	Leu	Leu	Val	Ser
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Ala	Leu	Gly	Met	Val	Pro	Pro	Pro	Glu	Asn	Val	Arg	Met	Asn	Ser	Val
			20					25					30		
Asn	Phe	Lys	Asn	Ile	Leu	Gln	Trp	Glu	Ser	Pro	Ala	Phe	Ala	Lys	Gly
		35				40						45			
Asn	Leu	Thr	Phe	Thr	Ala	Gln	Tyr	Leu	Ser	Tyr	Arg	Ile	Phe	Gln	Asp
	50					55					60				
Lys	Cys	Met	Asn	Thr	Thr	Leu	Thr	Glu	Cys	Asp	Phe	Ser	Ser	Leu	Ser
65					70					75				80	
Lys	Tyr	Gly	Asp	His	Thr	Leu	Arg	Val	Arg	Ala	Glu	Phe	Ala	Asp	Glu
			85					90						95	
His	Ser	Asp	Trp	Val	Asn	Ile	Thr	Phe	Cys	Pro	Val	Asp	Asp	Thr	Ile
			100					105						110	
Ile	Gly	Pro	Pro	Gly	Met	Gln	Val	Glu	Val	Leu	Asp	Asp	Ser	Leu	His
		115				120						125			
Met	Arg	Phe	Leu	Ala	Pro	Lys	Ile	Glu	Asn	Glu	Tyr	Glu	Thr	Trp	Thr
	130					135						140			
Met	Lys	Asn	Val	Tyr	Asn	Ser	Trp	Thr	Tyr	Asn	Val	Gln	Tyr	Trp	Lys
145					150					155				160	
Asn	Gly	Thr	Asp	Glu	Lys	Phe	Gln	Ile	Thr	Pro	Gln	Tyr	Asp	Phe	Glu
			165					170						175	
Val	Leu	Arg	Asn	Leu	Glu	Pro	Trp	Thr	Thr	Tyr	Cys	Val	Gln	Val	Arg
			180					185					190		
Gly	Phe	Leu	Pro	Asp	Arg	Asn	Lys	Ala	Gly	Glu	Trp	Ser	Glu	Pro	Val
		195					200						205		
Cys	Glu	Gln	Thr	Thr	His	Asp	Glu	Thr	Val	Pro	Ser	Gly	Ser	Gly	Ser
	210					215					220				
Gly	Ser	Gly	Ser	Glu	Pro	Arg	Ser	Ser	Asp	Lys	Thr	His	Thr	Cys	Pro
225					230					235				240	
Pro	Cys	Pro	Ala	Pro	Glu	Ala	Glu	Gly	Ala	Pro	Ser	Val	Phe	Leu	Phe
			245					250						255	

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val  
                   260                  265                  270  
 Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe  
                   275                  280                  285  
 Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro  
                   290                  295                  300  
 Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr  
 305                  310                  315                  320  
 Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val  
                   325                  330                  335  
 Ser Asn Lys Ala Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala  
                   340                  345                  350  
 Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg  
                   355                  360                  365  
 Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly  
                   370                  375                  380  
 Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro  
 385                  390                  395                  400  
 Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser  
                   405                  410                  415  
 Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln  
                   420                  425                  430  
 Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His  
                   435                  440                  445  
 Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Leu Val Pro Arg  
                   450                  455                  460  
 Gly Ser Gly Ser Gly Gly His His His His His His  
 465                  470                  475

&lt;210&gt; 24

&lt;211&gt; 63

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Oligonucleotide primer ZC29328

&lt;400&gt; 24

tcagagggat cgggttggg ttgggttcg gagccagat catcagacaa aactcacaca  
 tgc

60

63

&lt;210&gt; 25

<211> 65  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide primer ZC29231

<400> 25  
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 gggag 65

<210> 26  
 <211> 70  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide primer ZC39335

<400> 26  
 atcggaattc gcagaagcca tgaggacgct gctgaccatc ttgactgtgg ggtccctggc 60  
 tgctcacgcc 70

<210> 27  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide primer ZC28981

<400> 27  
 ttgggctcc ctgagctctg gtggaa 26

<210> 28  
 <211> 80  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide primer ZC39043

<400> 28

ctgactcag ctactccata ggcatatact cgccacctga tccggaacca cgcggaacca 60  
gtttaccgg aqacagggag 80

<210> 29

<211> 1452

<212> DNA

<213> Artificial Sequence

<220>

<223> hzcytor11 extracellular cytokine binding domain  
fused to IgG1 with a Glu-Glu tag

<221> CDS

<222> (1)...(1452)

<400> 29

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Met Arg Thr Leu Leu Thr Ile Leu Thr Val Gly Ser Leu Ala Ala His  
1 5 10 15

gcc cct gag gac ccc tgg gat ctg ctc cag cac gtg aaa ttc cag tcc 96  
Ala Pro Glu Asp Pro Ser Asp Leu Leu Gln His Val Lys Phe Gln Ser  
20 25 30

agc aac ttt gaa aac atc ctg acg tgg gac agc ggg cca gag ggc acc 144  
Ser Asn Phe Glu Asn Ile Leu Thr Trp Asp Ser Gly Pro Glu Gly Thr  
35 40 45

cca gac acg gtc tac agc atc gag tat aag acg tac gga gag agg gac 192  
Pro Asp Thr Val Tyr Ser Ile Glu Tyr Lys Thr Tyr Gly Glu Arg Asp  
50 55 60

tgg gtg gca aag aag ggc tgt cag cgg atc acc cgg aag tcc tgc aac 240  
Trp Val Ala Lys Lys Gly Cys Gln Arg Ile Thr Arg Lys Ser Cys Asn  
65 70 75 80

ctg acg gtg gag acg ggc aac ctc acg gag ctc tac tat gcc agg gtc 288  
Leu Thr Val Glu Thr Gly Asn Leu Thr Glu Leu Tyr Tyr Ala Arg Val  
85 90 95

acc gct gtc agt ggc gga ggc cgg tca gcc acc aag atg act gac agg 336  
Thr Ala Val Ser Ala Gly Gly Arg Ser Ala Thr Lys Met Thr Asp Arg  
100 105 110

ttc agc tct ctg cag cac act acc ctc aag cca cct gat gtg acc tgt	384
Phe Ser Ser Leu Gln His Thr Thr Leu Lys Pro Pro Asp Val Thr Cys	
115 120 125	
atc tcc aaa gtg aga tcg att cag atg att gtt cat cct acc ccc acg	432
Ile Ser Lys Val Arg Ser Ile Gln Met Ile Val His Pro Thr Pro Thr	
130 135 140	
cca atc cgt gca ggc gat ggc cac cgg cta acc ctg gaa gac atc ttc	480
Pro Ile Arg Ala Gly Asp Gly His Arg Leu Thr Leu Glu Asp Ile Phe	
145 150 155 160	
cal gac ctg ttc tac cac tta gag ctc cag gtc aac cgc acc tac caa	528
His Asp Leu Phe Tyr His Leu Glu Leu Gln Val Asn Arg Thr Tyr Gln	
165 170 175	
atg cac ctt gga ggg aag cag aga gaa tat gag ttc ttc ggc ctg acc	576
Met His Leu Gly Gly Lys Gln Arg Glu Tyr Glu Phe Phe Gly Leu Thr	
180 185 190	
cct gac aca gag ttc ctt ggc acc atc atg att tgc gtt ccc acc tgg	624
Pro Asp Thr Glu Phe Leu Gly Thr Ile Met Ile Cys Val Pro Thr Trp	
195 200 205	
gcc aag gag agt gcc ccc tac atg tgc cga gtg aag aca ctg cca gac	672
Ala Lys Glu Ser Ala Pro Tyr Met Cys Arg Val Lys Thr Leu Pro Asp	
210 215 220	
cgg aca tgg acc gga tcc ggt tcg ggt tcg ggt tcg gag ccc aga tca	720
Arg Thr Trp Thr Gly Ser Gly Ser Gly Ser Gly Ser Glu Pro Arg Ser	
225 230 235 240	
tca gac aaa act cac aca tgc cca cgg tgc cca gca cct gaa gcc gag	768
Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Glu	
245 250 255	
ggg gca cgg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc	816
Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu	
260 265 270	
atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc	864



Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser		
		275					280						285				
cac	gaa	gac	cct	gag	gtc	aag	ttc	aac	tgg	tac	gtg	gac	ggc	gtg	gag		912
His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu		
	290					295					300						
gtg	cat	aat	gcc	aag	aca	aag	ccg	cgg	gag	gag	cag	tac	aac	agc	acg		960
Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr		
305					310					315					320		
tac	cgt	gtg	gtc	agc	gtc	ctc	acc	gtc	ctg	cac	cag	gac	tgg	ctg	aal		1008
Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn		
				325					330					335			
ggc	aag	gag	tac	aag	tgc	aag	gtc	tcc	aac	aaa	gcc	ctc	cca	tcc	tcc		1056
Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ser	Ser		
		340					345					350					
atc	gag	aaa	acc	atc	tcc	aaa	gcc	aaa	ggg	cag	ccc	cga	gaa	cca	cag		1104
Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln		
	355					360					365						
gtg	tac	acc	ctg	ccc	cca	tcc	cgg	gat	gag	ctg	acc	aag	aac	cag	gtc		1152
Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val		
	370					375					380						
agc	ctg	acc	tgc	ctg	gtc	aaa	ggc	ttc	tat	ccc	agc	gac	atc	gcc	gtg		1200
Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val		
385					390					395					400		
gag	tgg	gag	agc	aat	ggg	cag	ccg	gag	aac	aac	tac	aag	acc	acg	cct		1248
Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro		
				405					410					415			
ccc	gtg	ctg	gac	tcc	gac	ggc	tcc	ttc	ttc	ctc	tac	agc	aag	ctc	acc		1296
Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr		
				420				425						430			
gtg	gac	aag	agc	agg	tgg	cag	cag	ggg	aac	gtc	ttc	tca	tgc	tcc	gtg		1344
Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val		
	435					440							445				

atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg 1392  
 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu  
 450 455 460

tct ccg ggt aaa ctg gtt ccg cgt ggt tcc gga tca ggt ggc gag tat 1440  
 Ser Pro Gly Lys Leu Val Pro Arg Gly Ser Gly Ser Gly Gly Glu Tyr  
 465 470 475 480

atg cct atg gag 1452  
 Met Pro Met Glu

<210> 30

<211> 484

<212> PRT

<213> Artificial Sequence

<400> 30

Met Arg Thr Leu Leu Thr Ile Leu Thr Val Gly Ser Leu Ala Ala His  
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 20 25 30  
 Ser Asn Phe Glu Asn Ile Leu Thr Trp Asp Ser Gly Pro Glu Gly Thr  
 35 40 45  
 Pro Asp Thr Val Tyr Ser Ile Glu Tyr Lys Thr Tyr Gly Glu Arg Asp  
 50 55 60  
 Trp Val Ala Lys Lys Gly Cys Gln Arg Ile Thr Arg Lys Ser Cys Asn  
 65 70 75 80  
 Leu Thr Val Glu Thr Gly Asn Leu Thr Glu Leu Tyr Tyr Ala Arg Val  
 85 90 95  
 Thr Ala Val Ser Ala Gly Gly Arg Ser Ala Thr Lys Met Thr Asp Arg  
 100 105 110  
 Phe Ser Ser Leu Gln His Thr Thr Leu Lys Pro Pro Asp Val Thr Cys  
 115 120 125  
 Ile Ser Lys Val Arg Ser Ile Gln Met Ile Val His Pro Thr Pro Thr  
 130 135 140  
 Pro Ile Arg Ala Gly Asp Gly His Arg Leu Thr Leu Glu Asp Ile Phe  
 145 150 155 160  
 His Asp Leu Phe Tyr His Leu Glu Leu Gln Val Asn Arg Thr Tyr Gln  
 165 170 175  
 Met His Leu Gly Gly Lys Gln Arg Glu Tyr Glu Phe Phe Gly Leu Thr  
 180 185 190

Pro Asp Thr Glu Phe Leu Gly Thr Ile Met Ile Cys Val Pro Thr Trp  
 195 200 205  
 Ala Lys Glu Ser Ala Pro Tyr Met Cys Arg Val Lys Thr Leu Pro Asp  
 210 215 220  
 Arg Thr Trp Thr Gly Ser Gly Ser Gly Ser Gly Ser Glu Pro Arg Ser  
 225 230 235 240  
 Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Glu  
 245 250 255  
 Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu  
 260 265 270  
 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser  
 275 280 285  
 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu  
 290 295 300  
 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr  
 305 310 315 320  
 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn  
 325 330 335  
 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ser Ser  
 340 345 350  
 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln  
 355 360 365  
 Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val  
 370 375 380  
 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val  
 385 390 395 400  
 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro  
 405 410 415  
 Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr  
 420 425 430  
 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val  
 435 440 445  
 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu  
 450 455 460  
 Ser Pro Gly Lys Leu Val Pro Arg Gly Ser Gly Ser Gly Gly Glu Tyr  
 465 470 475 480  
 Met Pro Met Glu

<210> 31

<211> 22

<212> DNA

<213> Artificial Sequence

&lt;220&gt;

&lt;223&gt; Oligonucleotide primer ZC37693

&lt;400&gt; 31

ccccagacac ggtctacagc at

22

&lt;210&gt; 32

&lt;211&gt; 23

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Oligonucleotide primer ZC37449

&lt;400&gt; 32

gggtcagggc gaagaactca tat

23

&lt;210&gt; 33

&lt;211&gt; 199

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 33

Met	Val	Pro	Pro	Pro	Glu	Asn	Val	Arg	Met	Asn	Ser	Val	Asn	Phe	Lys
1				5				10						15	
Asn	Ile	Leu	Gln	Trp	Glu	Ser	Pro	Ala	Phe	Ala	Lys	Gly	Asn	Leu	Thr
		20						25					30		
Phe	Thr	Ala	Gln	Tyr	Leu	Ser	Tyr	Arg	Ile	Phe	Gln	Asp	Lys	Cys	Met
		35						40					45		
Asn	Thr	Thr	Leu	Thr	Glu	Cys	Asp	Phe	Ser	Ser	Leu	Ser	Lys	Tyr	Gly
		50					55					60			
Asp	His	Thr	Leu	Arg	Val	Arg	Ala	Glu	Phe	Ala	Asp	Glu	His	Ser	Asp
65				70						75				80	
Trp	Val	Asn	Ile	Thr	Phe	Cys	Pro	Val	Asp	Asp	Thr	Ile	Ile	Gly	Pro
			85							90				95	
Pro	Gly	Met	Gln	Val	Glu	Val	Leu	Ala	Asp	Ser	Leu	His	Met	Arg	Phe
		100						105					110		
Leu	Ala	Pro	Lys	Ile	Glu	Asn	Glu	Tyr	Glu	Thr	Trp	Thr	Met	Lys	Asn
		115					120						125		
Val	Tyr	Asn	Ser	Trp	Thr	Tyr	Asn	Val	Gln	Tyr	Trp	Lys	Asn	Gly	Thr
		130					135						140		

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<210> 34
<211> 211
<212> PRT
<213> Homo sapiens
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Ser	Asp	Ala	His	Gly	Thr	Glu	Leu	Pro	Ser	Pro	Pro	Ser	Val	Trp	Phe
1				5				10						15	
Glu	Ala	Glu	Phe	Phe	His	His	Ile	Leu	His	Trp	Thr	Pro	Ile	Pro	Asn
			20					25					30		
Gln	Ser	Glu	Ser	Thr	Cys	Tyr	Glu	Val	Ala	Leu	Leu	Arg	Tyr	Gly	Ile
		35					40					45			
Glu	Ser	Trp	Asn	Ser	Ile	Ser	Asn	Cys	Ser	Gln	Thr	Leu	Ser	Tyr	Asp
	50					55					60				
Leu	Thr	Ala	Val	Thr	Leu	Asp	Leu	Tyr	His	Ser	Asn	Gly	Tyr	Arg	Ala
65					70					75					80
Arg	Val	Arg	Ala	Val	Asp	Gly	Ser	Arg	His	Ser	Asn	Trp	Thr	Val	Thr
				85					90					95	
Asn	Thr	Arg	Phe	Ser	Val	Asp	Glu	Val	Thr	Leu	Thr	Val	Gly	Ser	Val
			100					105					110		
Asn	Leu	Glu	Ile	His	Asn	Gly	Phe	Ile	Leu	Gly	Lys	Ile	Gln	Leu	Pro
		115					120					125			
Arg	Pro	Lys	Met	Ala	Pro	Ala	Asn	Asp	Thr	Tyr	Glu	Ser	Ile	Phe	Ser
	130					135					140				
His	Phe	Arg	Glu	Tyr	Glu	Ile	Ala	Ile	Arg	Lys	Val	Pro	Gly	Asn	Phe
145					150					155					160
Thr	Phe	Thr	His	Lys	Lys	Val	Lys	His	Glu	Asn	Phe	Ser	Leu	Leu	Thr
				165					170					175	
Ser	Gly	Glu	Val	Gly	Glu	Phe	Cys	Val	Gln	Val	Lys	Pro	Ser	Val	Ala
			180					185					190		
Ser	Arg	Ser	Asn	Lys	Gly	Met	Trp	Ser	Lys	Glu	Glu	Cys	Ile	Ser	Leu
		195					200					205			

